

FILE 'MEDLINE, BIOSIS, CAPLUS' ENTERED AT 15:01:12 ON 16 NOV 2006
L1 2214 S ABCG2 OR BCRP
L2 869 S INDOLOCARBAZOLE
L3 13 S L1 AND L2
L4 7 DUP REMOVE L3 (6 DUPLICATES REMOVED)

FILE 'STNGUIDE' ENTERED AT 15:03:11 ON 16 NOV 2006

FILE 'MEDLINE, BIOSIS, CAPLUS' ENTERED AT 15:05:48 ON 16 NOV 2006
L5 14029 S C421A OR 421
L6 25 S L1 AND L5
L7 11 DUP REMOVE L6 (14 DUPLICATES REMOVED)

EAST Search History

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	197	ABCG2 or BCRP	US-PGPUB; USPAT; USOCR	OR	ON	2006/11/16 14:55
L2	318083	snp or mutation or polymorphism or variant	US-PGPUB; USPAT; USOCR	OR	ON	2006/11/16 14:55
L3	134	L1 and L2	US-PGPUB; USPAT; USOCR	OR	ON	2006/11/16 14:56
L4	140707	"421" or C421A	US-PGPUB; USPAT; USOCR	OR	ON	2006/11/16 14:56
L5	24	L1 and L2 and L4	US-PGPUB; USPAT; USOCR	OR	ON	2006/11/16 14:58
L6	28	L1 and L4	US-PGPUB; USPAT; USOCR	OR	ON	2006/11/16 14:59
L7	335	indolocarbazole	US-PGPUB; USPAT; USOCR	OR	ON	2006/11/16 14:59
L8	4	L1 and L7 and L2	US-PGPUB; USPAT; USOCR	OR	ON	2006/11/16 15:00

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.14 [May-07-2006]

Match: 1 Mismatch: -2 gap open: 5 gap extension: 2

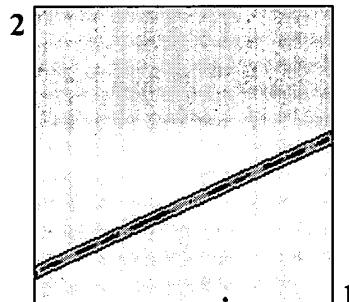
x_dropoff: 50 expect: 10.000 wordsize: 11 Filter View option StandardMasking character option X for protein, n for nucleotide Masking color option Black Show CDS translation Align

Sequence 1: gi|44847528|emb|CQ757490.1|Sequence 1 from Patent WO2003107249.

Length = 1968 (1 .. 1968)

Sequence 2: gi|62526032|ref|NM_004827.2|Homo sapiens ATP-binding cassette, sub-family G (WHITE), member 2 (ABCG2), mRNA

Length = 4445 (1 .. 4445)



NOTE: Bitscore and expect value are calculated based on the size of the nr database.

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence.

4445

Score = 3757 bits (1954), Expect = 0.0

Identities = 1968/1968 (100%), Gaps = 0/1968 (0%)

Strand=Plus/Plus

seq id #1

Query 1	ATGTCTTCCAGTAATGTCGAAGTTTATCCCAGTGTACAAGGAAACACCAATGGCTTC	60
Sbjct 494	ATGTCTTCCAGTAATGTCGAAGTTTATCCCAGTGTACAAGGAAACACCAATGGCTTC	553
Query 61	CCCGCGACAGCTCCAATGACCTGAAGGCATTTACTGAAGGGAGCTGTGTTAAGTTTCAT	120
Sbjct 554	CCCGCGACAGCTCCAATGACCTGAAGGCATTTACTGAAGGGAGCTGTGTTAAGTTTCAT	613
Query 121	AACATCTGCTATCGAGTAAAAGTGAAGAGTGGCTTCTACCTTGTGAAAACCAGTTGAG	180
Sbjct 614	AACATCTGCTATCGAGTAAAAGTGAAGAGTGGCTTCTACCTTGTGAAAACCAGTTGAG	673
Query 181	AAAGAAATATTATCGAATATCAATGGGATCATGAAACCTGGTCTAACGCCATCCTGGGA	240
Sbjct 674	AAAGAAATATTATCGAATATCAATGGGATCATGAAACCTGGTCTAACGCCATCCTGGGA	733
Query 241	CCCACAGGTGGAGGGCAAATCTCGTTATTAGATGTCTTAGCTGCAAGGAAAGATCCAAGT	300

Sbjct	734	CCCACAGGTGGAGGCAAATCTCGTTATTAGATGTCTTAGCTGCAAGGAAAGATCCAAGT	793
Query	301	GGATTATCTGGAGATGTTCTGATAAATGGAGCACCGCACCTGCCAATTCAAATGTAAT	360
Sbjct	794	GGATTATCTGGAGATGTTCTGATAAATGGAGCACCGCACCTGCCAATTCAAATGTAAT	853
Query	361	TCAGGTTACGTGGTACAAGATGATGTTGTGATGGCACCTGACGGTGAGAGAAAACCTTA	420
Sbjct	854	TCAGGTTACGTGGTACAAGATGATGTTGTGATGGCACCTGACGGTGAGAGAAAACCTTA	913
Query	421	CAGTTCTCAGCAGCTCTCGGCTTGCAACAACTATGACGAATCATGnnnnnnnCGAACGG	480
Sbjct	914	CAGTTCTCAGCAGCTCTCGGCTTGCAACAACTATGACGAATCATGAAAAAAACGAACGG	973
Query	481	ATTAACAGGGTCATTCAAGAGTTAGGTCTGGATAAAGTGGCAGACTCCAAGGTTGGAAC	540
Sbjct	974	ATTAACAGGGTCATTCAAGAGTTAGGTCTGGATAAAGTGGCAGACTCCAAGGTTGGAAC	1033
Query	541	CAGTTATCCGTGGTGTCTGGAGGAGAAAGAAAAAGGACTAGTATAGGAATGGAGCTT	600
Sbjct	1034	CAGTTATCCGTGGTGTCTGGAGGAGAAAGAAAAAGGACTAGTATAGGAATGGAGCTT	1093
Query	601	ATCACTGATCCTTCATCTTGTCTTGGATGAGCCTACAACTGGCTTAGACTCAAGCACA	660
Sbjct	1094	ATCACTGATCCTTCATCTTGTCTTGGATGAGCCTACAACTGGCTTAGACTCAAGCACA	1153
Query	661	GCAAATGCTGCTTTGCTCCTGAAAAGGATGTCTAACGCAGGGACGAACAATCATCTC	720
Sbjct	1154	GCAAATGCTGCTTTGCTCCTGAAAAGGATGTCTAACGCAGGGACGAACAATCATCTC	1213
Query	721	TCCATTCACTCAGCCTCGATATTCCATCTTCAAGTTGTTGATAGCCTCACCTTATTGGCC	780
Sbjct	1214	TCCATTCACTCAGCCTCGATATTCCATCTTCAAGTTGTTGATAGCCTCACCTTATTGGCC	1273
Query	781	TCAGGAAGACTTATGTTCCACGGGCCTGCTCAGGAGGCCTGGATACTTGAATCAGCT	840
Sbjct	1274	TCAGGAAGACTTATGTTCCACGGGCCTGCTCAGGAGGCCTGGATACTTGAATCAGCT	1333
Query	841	GGTTACTGACTGTGAGGCCTATAATAACCCCTGCAGACTTCTTCTGGACATCATTATGGA	900
Sbjct	1334	GGTTACTGACTGTGAGGCCTATAATAACCCCTGCAGACTTCTTCTGGACATCATTATGGA	1393
Query	901	GATTCACACTGCTGTGGCATTAAACAGAGAAGAAGACTTTAAAGCCACAGAGATCATAGAG	960
Sbjct	1394	GATTCACACTGCTGTGGCATTAAACAGAGAAGAAGACTTTAAAGCCACAGAGATCATAGAG	1453
Query	961	CCTTCCAAGCAGGATAAGCCACTCATAGAAAAATTAGCGGAGATTATGTCAACTCCTCC	1020
Sbjct	1454	CCTTCCAAGCAGGATAAGCCACTCATAGAAAAATTAGCGGAGATTATGTCAACTCCTCC	1513
Query	1021	TTCTACAAAGAGACAAAGCTGAATTACATCAACTTCCGGGGGTGAGAAGAAGAAGAAG	1080
Sbjct	1514	TTCTACAAAGAGACAAAGCTGAATTACATCAACTTCCGGGGGTGAGAAGAAGAAGAAG	1573
Query	1081	ATCACAGTCTCAAGGAGATCAGCTACACCACCTCCTCTGTCTCAACTCAGATGGTT	1140
Sbjct	1574	ATCACAGTCTCAAGGAGATCAGCTACACCACCTCCTCTGTCTCAACTCAGATGGTT	1633
Query	1141	TCCAAGCGTTATTCAAAACTTGCTGGTAATCCCCAGGCCTCTATAGCTCAGATCATT	1200
Sbjct	1634	TCCAAGCGTTATTCAAAACTTGCTGGTAATCCCCAGGCCTCTATAGCTCAGATCATT	1693
Query	1201	GTCACAGTCGTACTGGACTGGTTATAGGTGCCATTACTTGGCTAAAAATGATTCT	1260
Sbjct	1694	GTCACAGTCGTACTGGACTGGTTATAGGTGCCATTACTTGGCTAAAAATGATTCT	1753

Query	1261	ACTGGAATCCAGAACAGAGCTGGGTTCTCTTCTTGACGACCAACCAGTGTTCAGC	1320
Sbjct	1754	ACTGGAATCCAGAACAGAGCTGGGTTCTCTTCTTGACGACCAACCAGTGTTCAGC	1813
Query	1321	AGTGTTCAGCGTGGAACTCTTGTGGTAGAGAAGAAGCTTCATACATGAATACATC	1380
Sbjct	1814	AGTGTTCAGCGTGGAACTCTTGTGGTAGAGAAGAAGCTTCATACATGAATACATC	1873
Query	1381	AGCGGATACTACAGAGTGTACATTCTTCTTGAAAAGTGTATCTGATTATTACCC	1440
Sbjct	1874	AGCGGATACTACAGAGTGTACATTCTTCTTGAAAAGTGTATCTGATTATTACCC	1933
Query	1441	ATGAGGATGTTACCAAGTATTATATTACCTGTATAGTGTACTTCATGTTAGGATTGAAG	1500
Sbjct	1934	ATGAGGATGTTACCAAGTATTATATTACCTGTATAGTGTACTTCATGTTAGGATTGAAG	1993
Query	1501	CCAAAGGCAGATGCCTCTCGTTATGATGTTACCTTATGATGGGGTTATTAGCC	1560
Sbjct	1994	CCAAAGGCAGATGCCTCTCGTTATGATGTTACCTTATGATGGGGTTATTAGCC	2053
Query	1561	AGTTCCATGGCACTGCCATAGCAGCAGGTCAAGGTGTGGTTCTGTAGCAACACTTC	1620
Sbjct	2054	AGTTCCATGGCACTGCCATAGCAGCAGGTCAAGGTGTGGTTCTGTAGCAACACTTC	2113
Query	1621	ATGACCATCTGTTGTGTTATGATGATTTTCAGGTCTGTTGGTCAATCTCACACC	1680
Sbjct	2114	ATGACCATCTGTTGTGTTATGATGATGATTTTCAGGTCTGTTGGTCAATCTCACACC	2173
Query	1681	ATTGCATCTGGCTGTACGGCTTCAGTACTTCAGCATCCACGATATGGATTACGGCT	1740
Sbjct	2174	ATTGCATCTGGCTGTACGGCTTCAGTACTTCAGCATCCACGATATGGATTACGGCT	2233
Query	1741	TTGCAGCATAATGAATTTGGACAAAAGTCTGCCAGGACTCAATGCAACAGGAAAC	1800
Sbjct	2234	TTGCAGCATAATGAATTTGGACAAAAGTCTGCCAGGACTCAATGCAACAGGAAAC	2293
Query	1801	AATCCTTGTAACTATGCAACATGTACTGGCGAAGAATATTGGTAAAGCAGGGCATCGAT	1860
Sbjct	2294	AATCCTTGTAACTATGCAACATGTACTGGCGAAGAATATTGGTAAAGCAGGGCATCGAT	2353
Query	1861	CTCTCACCTGGGCTTGTGGAAGAATCACGTGCCCTGGCTGTATGATTGTTATTTC	1920
Sbjct	2354	CTCTCACCTGGGCTTGTGGAAGAATCACGTGCCCTGGCTGTATGATTGTTATTTC	2413
Query	1921	CTCACAAATTGCCTACCTGAAATTGTTATTCTTAAAAAATTCTTAA	1968
Sbjct	2414	CTCACAAATTGCCTACCTGAAATTGTTATTCTTAAAAAATTCTTAA	2461

CPU time: 0.03 user secs. 0.01 sys. secs 0.04 total secs.

Lambda K H
1.33 0.621 1.12

Gapped Lambda K H
1.33 0.621 1.12

Matrix: blastn matrix:1 -2
 Gap Penalties: Existence: 5, Extension: 2
 Number of Sequences: 1
 Number of Hits to DB: 608
 Number of extensions: 9
 Number of successful extensions: 1
 Number of sequences better than 10.0: 1

Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Length of query: 1968
Length of database: 18,419,680,154
Length adjustment: 27
Effective length of query: 1941
Effective length of database: 18,419,680,127
Effective search space: 35752599126507
Effective search space used: 35752599126507
X1: 11 (21.1 bits)
X2: 26 (50.0 bits)
X3: 26 (50.0 bits)
S1: 15 (29.5 bits)
S2: 22 (43.0 bits)